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JP18 1652

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/534,229C

DATE: 04/12/2002
TIME: 15:08:05

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\04122002\I534229C.raw

ENTERED

5 <110> APPLICANT: Kawakami, Akira
 6 Terami, Fumihiro
 9 <120> TITLE OF INVENTION: LOW TEMPERATURE EXPRESSION CHITINASE CDNAS AND METHOD FOR
 ISOLATING THE
 10 SAME
 13 <130> FILE REFERENCE: 107156-00004
 W--> 14 <140> CURRENT APPLICATION NUMBER: US 09/534,229C
 16 <141> CURRENT FILING DATE: 2000-03-24
 19 <160> NUMBER OF SEQ ID NOS: 8
 22 <170> SOFTWARE: PatentIn version 3.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 256
 27 <212> TYPE: PRT
 28 <213> ORGANISM: Triticum aestivum
 31 <400> SEQUENCE: 1
 33 Met Ala Arg Phe Ala Ala Leu Ala Val Cys Ala Ala Ala Leu Leu Leu
 34 1 5 10 15
 36 Ala Val Ala Ala Gly Gly Ala Ala Ala Gln Gly Val Gly Ser Val Ile
 37 20 25 30
 39 Thr Arg Ser Val Tyr Ala Ser Met Leu Pro Asn Arg Asp Asn Ser Leu
 40 35 40 45
 42 Cys Pro Ala Arg Gly Phe Tyr Thr Tyr Asp Ala Phe Ile Ala Ala Ala
 43 50 55 60
 45 Asn Thr Phe Pro Gly Phe Gly Thr Thr Gly Ser Ala Asp Asp Ile Lys
 46 65 70 75 80
 48 Arg Asp Leu Ala Ala Phe Phe Gly Gln Thr Ser His Glu Thr Thr Gly
 49 85 90 95
 51 Gly Thr Arg Gly Ala Ala Asp Gln Phe Gln Trp Gly Tyr Cys Phe Lys
 52 100 105 110
 54 Glu Glu Ile Ser Lys Ala Thr Ser Pro Pro Tyr Tyr Gly Arg Gly Pro
 55 115 120 125
 57 Ile Gln Leu Thr Gly Arg Ser Asn Tyr Asp Leu Ala Gly Arg Ala Ile
 58 130 135 140
 60 Gly Lys Asp Leu Val Ser Asn Pro Asp Leu Val Ser Thr Asp Ala Val
 61 145 150 155 160
 63 Val Ser Phe Arg Thr Ala Met Trp Phe Trp Met Thr Ala Gln Gly Asn
 64 165 170 175
 66 Lys Pro Ser Cys His Asn Val Ala Leu Arg Arg Trp Thr Pro Thr Ala
 67 180 185 190
 69 Ala Asp Thr Ala Ala Gly Arg Val Pro Gly Tyr Gly Val Ile Thr Asn
 70 195 200 205
 72 Ile Ile Asn Gly Gly Leu Glu Cys Gly Met Gly Arg Asn Asp Ala Asn
 73 210 215 220
 75 Val Asp Arg Ile Gly Tyr Tyr Thr Arg Tyr Cys Gly Met Leu Gly Thr

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76	225	230	235	240
78	Ala Thr Gly Gly Asn Leu Asp Cys Tyr Thr Gln Arg Asn Phe Ala Ser			
79		245	250	255
81	<210> SEQ ID NO: 2			
82	<211> LENGTH: 323			
83	<212> TYPE: PRT			
84	<213> ORGANISM: Triticum aestivum			
87	<400> SEQUENCE: 2			
89	Met Ser Thr Leu Arg Ala Arg Cys Ala Thr Ala Val Leu Ala Val Val			
90	1	5	10	15
92	Leu Ala Ala Ala Ala Val Thr Pro Ala Thr Ala Glu Gln Cys Gly Ser			
93		20	25	30
95	Gln Ala Gly Gly Ala Lys Cys Ala Asp Cys Leu Cys Cys Ser Gln Phe			
96		35	40	45
98	Gly Phe Cys Gly Thr Thr Ser Asp Tyr Cys Gly Pro Arg Cys Gln Ser			
99		50	55	60
101	Gln Cys Thr Gly Cys Gly Gly Gly Gly Val Ala Ser Ile Val			
102	65	70	75	80
104	Ser Arg Asp Leu Phe Glu Arg Phe Leu Leu His Arg Asn Asp Ala Ala			
105		85	90	95
107	Cys Leu Ala Arg Gly Phe Tyr Thr Tyr Asp Ala Phe Leu Ala Ala Ala			
108		100	105	110
110	Gly Ala Phe Pro Ala Phe Gly Thr Thr Gly Asp Leu Asp Thr Arg Lys			
111		115	120	125
113	Arg Glu Val Ala Ala Phe Phe Gly Gln Thr Ser His Glu Thr Thr Gly			
114		130	135	140
116	Gly Trp Pro Thr Ala Pro Asp Gly Pro Phe Ser Trp Gly Tyr Cys Phe			
117	145	150	155	160
119	Lys Gln Glu Gln Gly Ser Pro Pro Ser Tyr Cys Asp Gln Ser Ala Asp			
120		165	170	175
122	Trp Pro Cys Ala Pro Gly Lys Gln Tyr Tyr Gly Arg Gly Pro Ile Gln			
123		180	185	190
125	Leu Thr His Asn Tyr Asn Tyr Gly Pro Ala Gly Arg Ala Ile Gly Val			
126		195	200	205
128	Asp Leu Leu Asn Asn Pro Asp Leu Val Ala Thr Asp Pro Thr Val Ala			
129		210	215	220
131	Phe Lys Thr Ala Ile Trp Phe Trp Met Thr Thr Gln Ser Asn Lys Pro			
132	225	230	235	240
134	Ser Cys His Asp Val Ile Thr Gly Leu Trp Thr Pro Thr Ala Arg Asp			
135		245	250	255
137	Ser Ala Ala Gly Arg Val Pro Gly Tyr Gly Val Ile Thr Asn Val Ile			
138		260	265	270
140	Asn Gly Gly Ile Glu Cys Gly Met Gly Gln Asn Asp Lys Val Ala Asp			
141		275	280	285
143	Arg Ile Gly Phe Tyr Lys Arg Tyr Cys Asp Ile Phe Gly Ile Gly Tyr			
144		290	295	300
146	Gly Asn Asn Leu Asp Cys Tyr Asn Gln Leu Ser Phe Asn Val Gly Leu			
147	305	310	315	320
149	Ala Ala Gln			

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Input Set : A:\PTO.VSK.txt
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152 <210> SEQ ID NO: 3
153 <211> LENGTH: 319
154 <212> TYPE: PRT
155 <213> ORGANISM: Triticum aestivum
158 <400> SEQUENCE: 3
160 Met Arg Gly Val Val Val Ala Met Leu Ala Ala Ala Phe Ala Val
161 1 5 10 15
163 Ser Ala His Ala Glu Gln Cys Gly Ser Gln Ala Gly Gly Ala Thr Cys
164 20 25 30
166 Pro Asn Cys Leu Cys Cys Ser Lys Phe Gly Phe Cys Gly Thr Thr Ser
167 35 40 45
169 Asp Tyr Cys Gly Thr Gly Cys Gln Ser Gln Cys Asn Gly Cys Ser Gly
170 50 55 60
172 Gly Thr Pro Val Pro Val Pro Thr Pro Ser Gly Gly Gly Val Ser Ser
173 65 70 75 80
175 Ile Ile Ser Gln Ser Leu Phe Asp Gln Met Leu Leu His Arg Asn Asp
176 85 90 95
178 Ala Ala Cys Leu Ala Lys Gly Phe Tyr Asn Tyr Gly Ala Phe Val Ala
179 100 105 110
181 Ala Ala Asn Ser Phe Ser Gly Phe Ala Thr Thr Gly Ser Thr Asp Val
182 115 120 125
184 Lys Lys Arg Glu Val Ala Ala Phe Leu Ala Gln Thr Ser His Glu Thr
185 130 135 140
187 Thr Gly Gly Trp Pro Thr Ala Pro Asp Gly Pro Tyr Ser Trp Gly Tyr
188 145 150 155 160
190 Cys Phe Asn Gln Glu Arg Gly Ala Thr Ser Asp Tyr Cys Thr Pro Ser
191 165 170 175
193 Ser Gln Trp Pro Cys Ala Pro Gly Lys Lys Tyr Phe Gly Arg Gly Pro
194 180 185 190
196 Ile Gln Ile Ser His Asn Tyr Asn Tyr Gly Pro Ala Gly Gln Ala Ile
197 195 200 205
199 Gly Thr Asp Leu Leu Asn Asn Pro Asp Leu Val Ala Ser Asp Ala Thr
200 210 215 220
202 Val Ser Phe Lys Thr Ala Leu Trp Phe Trp Met Thr Pro Gln Ser Pro
203 225 230 235 240
205 Lys Pro Ser Ser His Asp Val Ile Thr Gly Arg Trp Ser Pro Ser Gly
206 245 250 255
208 Ala Asp Gln Ala Ala Gly Arg Val Pro Gly Tyr Gly Val Ile Thr Asn
209 260 265 270
211 Ile Ile Asn Gly Gly Leu Glu Cys Gly Arg Gly Gln Asp Gly Arg Val
212 275 280 285
214 Ala Asp Arg Ile Gly Phe Tyr Lys Arg Tyr Cys Asp Leu Leu Gly Val
215 290 295 300
217 Ser Tyr Gly Asp Asn Leu Asp Cys Tyr Asn Gln Arg Pro Phe Ala
218 305 310 315
220 <210> SEQ ID NO: 4
221 <211> LENGTH: 23
222 <212> TYPE: DNA

C--> 223 <213> ORGANISM: Artificial

RAW SEQUENCE LISTING
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Input Set : A:\PTO.VSK.txt
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226 <220> FEATURE:
227 <221> NAME/KEY: misc_feature
228 <222> LOCATION: (1)..(23)
229 <223> OTHER INFORMATION: Artificial primer.
232 <220> FEATURE:
233 <221> NAME/KEY: misc_feature
234 <222> LOCATION: 12, 18
235 <223> OTHER INFORMATION: n can be one of a,c,t, or g
238 <400> SEQUENCE: 4

 239 cacgagacca cnngcggntg ggc 23

242 <210> SEQ ID NO: 5
243 <211> LENGTH: 20
244 <212> TYPE: DNA

C--> 245 <213> ORGANISM: Artificial

249 <220> FEATURE:
250 <221> NAME/KEY: misc_feature
251 <222> LOCATION: (1)..(20)
252 <223> OTHER INFORMATION: Artificial primer.
255 <220> FEATURE:
256 <221> NAME/KEY: misc_feature
257 <222> LOCATION: 3
258 <223> OTHER INFORMATION: n can be one of a,c,t, or g

 261 <400> SEQUENCE: 5 20

262 acnaatatca tcaacggcg 20
265 <210> SEQ ID NO: 6
266 <211> LENGTH: 771
267 <212> TYPE: DNA
268 <213> ORGANISM: Triticum aestivum
271 <220> FEATURE:
272 <221> NAME/KEY: misc_feature
273 <222> LOCATION: (1)..(771)
274 <223> OTHER INFORMATION: cDNA
277 <400> SEQUENCE: 6

278 atggcgaggt ttgctgccct cggcggtgtgc gccggcgcc tcctgctcgc cgtggcgccg	60
280 ggggggtgcgg cggcgcaggg cgtgggctcg gtcatcacgc ggtcgggtga cgcgagcact	120
282 ctgccccaaacc gcgacaactc gctgtgcccgg ccagagggt tctacacgta cgacgccttc	180
284 atcgccgccc ccaacacccctt cccgggcttc ggcaccacccg gcagcgccga cgacatcaag	240
286 cgcgacctcg ccgccttctt cggccagacc tcccacgaga ccaccggagg gacgagaggc	300
288 gctgccgacc agttccagtg gggctactgc ttcaaggaag agataagcaa ggccacgtcc	360
290 ccaccatact atggacgggg acccatccaa ttgacagggc ggtccaacta cgatttgcc	420
292 gggagagcga tcgggaagga cttggtgagc aaccacgacc tagtgtccac ggacgcggtg	480
294 gtgtccttca ggacggccat gtggttctgg atgacggcgc agggaaaacaa gccgtcgtgc	540
296 cacaacgtcg ccctacgccc ctggacgccc acggccgccc acaccgctgc cggcagggtta	600
298 cccggatacg gagtgatcac caatatcatc aacggcgggc tcgagtgccg aatggggccgg	660
300 aacgacgcca acgtcgaccg catcggtac tacacgcgt actgcggcat gctggcaccg	720
302 gccacccggag gcaacccatcgat ctgctacacc cagaggaact tcgcttagcta g	771

305 <210> SEQ ID NO: 7
306 <211> LENGTH: 972
307 <212> TYPE: DNA

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308 <213> ORGANISM: Triticum aestivum
 311 <220> FEATURE:
 312 <221> NAME/KEY: misc_feature
 313 <222> LOCATION: (1)..(972)
 314 <223> OTHER INFORMATION: cDNA
 317 <400> SEQUENCE: 7

318	atgtccacgc tgagagcgcg gtgtgcgacg gccgtcctgg c cg t c g t c c t gg c g g c g g c c	60
320	g c g g t c a c g c c g g c a c a g g c c g a g c a g t g c g g c a a g t g c g c c	120
322	g a c t g c c t g t g c t g c a g c c a g t g c a c c a c t c c c g a c t a c t g c g g c c c	180
324	c g c t g c c a g a g c c a g t g c a c t g c g g t g c g g c g g c g g g g g t g c c t c a t c t g	240
326	t c c a g g g a c c a c t g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c	300
328	g g g t t c t a c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c	360
330	a c c g g a g a c c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c	420
332	g a g a c c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c	480
334	a a g c a g g a g a g g c t c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c	540
336	c c c g g c a a g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c	600
338	c c g g c g g g c c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c	660
340	c c g a c a g t g g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c	720
342	t c g t g c c a t g a c g t g a c t g a c t g a c t g a c t g a c t g a c t g a c t g a c t g a c t g a	780
344	c g g g t a c c c g g g t a c c c a a c a c t c a a c a c t c a a c a c t c a a c a a g c c a a g c c	840
346	g g g c a g a a c g a c a a g g t g g c a c a a g g t g g c a c a a g g t g g c a c a a g g t g g c a c a a g g c	900
348	g g c a t c g g c t a c g g a a t a a c c a a c t g a c t g a c t g a c t g a c t g a c t g a c t g a c t g a	960
350	g c g g c a c a g t g a c t g a c t g a c t g a c t g a c t g a c t g a c t g a c t g a c t g a c t g a c t g a	972
353	<210> SEQ ID NO: 8	
354	<211> LENGTH: 960	
355	<212> TYPE: DNA	
356	<213> ORGANISM: Triticum aestivum	
360	<220> FEATURE:	
361	<221> NAME/KEY: misc_feature	
362	<222> LOCATION: (1)..(960)	
363	<223> OTHER INFORMATION: cDNA	
366	<400> SEQUENCE: 8	
367	a t g a g a g g a g t t g g t g g t g g c a t g c t g g c c g g g c c t c g c c t g t g c t g c a c g c c	60
369	g a g c a a t g c g g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a a g	120
371	t t c g g t t c t g c g c a c c a c t c c g a c t a c t g c g c a c c g g c a c g c a a g t g c a a t	180
373	g g c t g c a c g c g g c a c c c c c g g t a c c g g t a c c g a c c c c c c g g c g g c g g c g g c g g c	240
375	a t t a t c t c g c a g t c g c t t c a c c a g a t g c t g c a c c g a c g c a c g c a c g c a c g c a c g c	300
377	g c c a a g g g t t c t a c a a c t a c c g c c t t c g c c c g c c g c c g c c g c c g c c g c c g c c g c	360
379	g c g a c c a c a g g t a c c c a c c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c	420
381	t c c c a c g a g a c a c c g g c g g t g g c c a c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c	480
383	t g c t t c a a c c a g g a g g c g g c g g c a c c g c a c g c a c g c a c g c a c g c a c g c a c g c a c g c	540
385	t g t g c g c c g g g c a a g a g t a c c c g g c g g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c	600
387	t a c g g g c c g g g c g g g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c	660
389	t c g g a c g c g a g g t a c c c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c	720
391	a a g c t t c g a g g a g g t a c c c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c	780
393	g c g g g g a g g g t a c c c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c	840
395	g g g c g c g g g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c	900
397	c t c c t t g g c g g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c a c c g c	960

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/534,229C

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; N Pos. 12,18

Seq#:5; N Pos. 3

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:4,5

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/534,229B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping".
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each Jth amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial-Sequence
- 11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.